

OM of: US-08-711-417C-165 to: Pending_Patents_AA_Main.* out_format : pfs

Date: Aug 28, 2002 10:13 AM

About: Results were produced by the GenCore software, version 4.5,
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Command line parameters:

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-MODEL=frame+np2.model -DEV=xlp
-Q/cgn2_1/USPTO_spool/6228611/runat_28082002_100211_13594/app_query.fasta_1.1639
-DB=Pending_Patents_AA_Main -OFM=fastan -SUFFIX=rapm
-GAPOP=12.000 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPEXT=0.000
-LOOPEXT=0.000 -GAPEXT=4.500 -GAPEXT=0.050 -GAPEXT=0.000
-LOOPEXT=0.500 -GAPEXT=6.000 -GAPEXT=7.000 -GAPEXT=10.000
-DELOP=0.500 -DELOP=6.000 -DELOP=7.000 -START=1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCLIGN=200
-THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pfs -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=6228611.ecn1_1.784 -NCPU=6 -ICPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLIPX -WAIT -THREADS=1
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Search information block:

Query: US-08-711-417C-165

Query length: 1551

Database: Pending_Patents_AA_Main.*

Database sequence: 351980561

Database length: 351980561

Search time (sec): 370.380000

score_list:

Sequence	Strd Orig	zScore	EScore Len	Documentation
/cgn2_6/ptodata/2/paa/PCRTUS_COMB.ppt:US99-02559-25	2467.00	2936.88	1.3e-155	461
/cgn2_6/ptodata/2/paa/US090_COMB.ppt:US-09-019-348-25	2467.00	2936.88	1.3e-155	461
/cgn2_6/ptodata/2/paa/US090_COMB.ppt:US-09-019-348-25	2467.00	2936.88	1.3e-155	461
/cgn2_6/ptodata/2/paa/US097_COMB.ppt:US-09-755-830-38	2467.00	2936.88	1.3e-155	461
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/cgn2_6/ptodata/2/paa/US090_COMB.ppt:US-09-019-348-27	2437.00	2899.93	1.4e-153	518
/cgn2_6/ptodata/2/paa/US090_COMB.ppt:US-09-019-348A-27	2437.00	2899.93	1.4e-153	518
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/cgn2_6/ptodata/2/paa/PCRTUS_COMB.ppt:US99-04224-7	2426.50	2887.42	6.7e-153	517
/cgn2_6/ptodata/2/paa/US081_COMB.ppt:US-08-121-438-5	2422.00	2887.14	1.4e-152	568
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/cgn2_6/ptodata/2/paa/US084_COMB.ppt:US-08-465-5908-153	2207.50	2626.84	2.4e-138	470
/cgn2_6/ptodata/2/paa/US087_COMB.ppt:US-08-733-6228-22	2207.50	2626.84	2.4e-138	470
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/cgn2_6/ptodata/2/paa/US090_COMB.ppt:US-09-019-348-26	1963.00	2335.71	4.3e-122	432
/cgn2_6/ptodata/2/paa/US097_COMB.ppt:US-09-755-830-39	1963.00	2335.71	4.3e-122	432
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/cgn2_6/ptodata/2/paa/US090_COMB.ppt:US-09-019-348A-24	1923.50	2288.57	1.8e-119	431
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/cgn2_6/ptodata/2/paa/US090_COMB.ppt:US-09-019-348-28	1681.00	1999.98	2.4e-103	390
/cgn2_6/ptodata/2/paa/US097_COMB.ppt:US-09-755-830-41	1681.00	1999.98	2.4e-103	390
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/cgn2_6/ptodata/2/paa/US097_COMB.ppt:US-09-755-830-42	1625.00	1933.47	1.3e-99	376
/cgn2_6/ptodata/2/paa/US087_COMB.ppt:US-08-733-622B-27	1556.00	1852.94	4.7e-95	310

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/cgn2_6/ptodata/2/paa/PCRTUS_COMB.ppt:US99-04224-6 + 1369.00 1624.56 1.5e-82 52
/cgn2_6/ptodata/2/paa/US092_COMB.ppt:US-09-259-389-6 + 1369.00 1624.56 1.5e-82 52
/cgn2_6/ptodata/2/paa/US60_COMB.ppt:US-60-243-468-1020 + 1309.00 1552.25 1.4e-78 5
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seq_documentation_block:
; Sequence 25, Application PC/TUS9902559
; GENERAL INFORMATION:
; APPLICANT: Shiseido Co., Ltd.
; TITLE OF INVENTION: AIOLOS GENE
; FILE REFERENCE: 10287/031W01
; CURRENT APPLICATION NUMBER: PCT/US99/02559
; EARLIER FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: US 09/019,348
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US99-02559-25
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alignment_scores:
Quality: 2467.00 Length: 461
Ratio: 5.351 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

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US-08-711-417C-165 x PCT-US99-02559-25
Align seg 1/1 to: PCT-US99-02559-25 from: 1 to: 461

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1 AsnValLysValGluThrGlnSerAspGluAsnGlyArgAlaCysG1 17

216 AATGAATGGGGAAGAATGTGGGAGGATTACGAATGCTGATCCCTCGG 265
|||||
17 uMetAsnGlyGluGluCysAlaGluAspLeuArgMetLeuAspAlaSerG 34

266 GAGAGAAATGAATGGCTCCACAGGACCAAGCAGCTCGGCTTTCGCG 315
|||||
34 lGluLysMetAsnGlySerHisArgAspGlnGlySerSerAlaLeuSer 50

316 GGAGTTGGAGGACATTCGACTTCCTAACGGRAAACTAAGTGTGATATCG 365
|||||
51 GlyValGlyGlyIleArgLeuProAsnGlyLysLeuLysCysAspIleCy 67

366 TGGGATCATTTGCTCGGGCCCAATGTGCTCATGTTTCACAAAAGAAGCC 415
|||||
67 sGlyIleLeuLysGlyProAsnValLeuMetValHisLysArgSerH 84

416 ACAGTGGAGAACGGCCCTTCAGTGTCAATCAGTCGGGGGCTCATTCACC 465
|||||
84 lThrGlyGluArgProPheGlnCysAsnGlnCysGlyAlaSerPheThr 100

466 CAGAGGGCAACCTGCTCCGGCCACATCAAGCTGCATTCGGGGGAGAAGCC 515
|||||
101 GlnLysGlyAsnLeuLeuArgHisIleLysLeuHisSerGlyGluTyPr 117

516 CTTCAATGCTCCTGCAACTACGCTTCGGCCGCGGAGGACGCCCTCA 565
|||||
117 oPhelysCysHisLeuLysCysAsnTyrAlaCysArgArgAspAlaLeuT 134

566 CTGGCCACCTGAGGACGACCTCCGTTGGTAAACCTCAAAATGTGGATAT 615
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134 hrGlyHisLeuArgThrHisSerValGlyLysProHisLysCysGlyTyr 150
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666 CTGCCCAACTACTTGGAAAGCATGGGCTTCGGGCGACACTGTACCCAG 715
|||||
167 gCysHisAsnTyrLeuGluSerMetGlyLeuProGlyThrLeuTyrProV 184
716 TCATTAAAGAAGAACTAAGCAGCAGTGAATGGCAGAGACCTGTGCAAG 765
|||||
184 alileysGluGluThrLysHisSerGluMetAlaGluAspLeucysLys 200
766 ATAGGATCAGAGAGATCTCTCGCTGGACAGACTAGCAAGTAATGTGC 815
|||||
201 IleGlySerGluArgSerLeuValLeuAspArgLeuAlaSerAsnValAl 217
816 CAAACGTAGAGCTCTATGCCCTCAGAAATTTCTGGGACAGGCGCTGT 865
|||||
217 aLysArgLysSerSerMetProGlnLysPheLeuGlyAspLysGlyLeu 234
866 CGCACAGCGCCTACGACAGTGCACGTACGAGAGGAGAACCAATGATG 915
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234 erAspThrProTyrAspSerAlaThrTyrGluLysGluAsnGluMetMet 250
916 AGTCCCGCTGATGACCAAGCCATCAACACGCCATCACTACTGGG 965
|||||
251 LysSerHisValMetAspGlnAlaIleAsnAsnAlaIleAsnTyrLeuGl 267
966 GCGCGAGTCCCTGCGCCGCTGTGTCAGACGCCCGCGGCTTCGAGG 1015
|||||
267 yAlaGluSerLeuArgProLeuValGlnThrProProGlyGlySerGluV 284
1016 TGTGCCCGCTCATACGCCGATGTACAGCTGCACAGGCGCTCGGAGGCG 1065
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284 alValProValIleSerProMetTyrGlnLeuHisArgArgSerGluGly 300
1066 ACCCGCGCTCAACCACTCGGCCAGGACAGCGCGGTGGAGTACTGCT 1115
|||||
301 ThrProArgSerAsnHisSerAlaGlnAspSerAlaValGluTyrLeuLe 317
1116 GTGCTCTCCAAAGGCCAAGTTGGTCCCTCGCGAGCGCGGCTCCCGA 1165
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317 uLeuLeuSerLysAlaLysLeuValProSerGluArgGluAlaSerProS 334
1166 GCAACAGCTGCCAAGACTCCAGCACCGGAGAGCAACACAGGAGGAG 1215
|||||
334 erAsnSerCysGlnAspSerThrAspThrGluSerAsnAsnGluGluGln 350
1216 CGCAGCGGTCTTATCTACCTGACCAACACATCGCCCGACGCGCGCAAG 1265
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351 ArgSerGlyLeuIleTyrLeuThrAsnHisIleAlaArgAlaGlnAr 367
1266 CTGTGCTCAAGGAGGAGCACCGGCTTACGACCTGCTGCGCGCGCT 1315
|||||
367 gValSerLeuLysGluGluHisArgAlaTyrAspLeuLeuArgAlaAla 384
1316 CCGAGAACTCGCAGGACGCGCTCCGCGGTGTCAGCACACAGCGGGAG 1365
|||||
384 erGluAsnSerGlnAspAlaLeuArgValValSerThrSerGlyGluGln 400
1366 ATGAGAGTGTACAAGTGGGAACACTCGCGGTGCTCTTCCTGGATCAGT 1415
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401 MetLysValTyrLysCysGluHisCysArgValLeuPheLeuAspHisVa 417
1416 CATGTACACCATCCACATGGGTGCGACGGCTTCGCTGATCCTTTTGTAGT 1465
|||||
417 lMetTyrThrIleHisMetGlyCysHisGlyPheArgAspPropheGluC 434
1466 GCAACATGTGCGGCTACCAAGCCAGGACCGGTACGAGTCTTCGTGCGAC 1515
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1516 ATAACGCGAGGGGACCGCTTCACATGAGC 1548
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451 IleThrArgGlyGluHisArgPheHisMetSer 461
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seq_documentation_block:
; Sequence 25, Application US/09019348
; GENERAL INFORMATION:
; APPLICANT: Georgopoulos, Katia
; APPLICANT: Morgan, Bruce
; TITLE OF INVENTION: AIOLOS GENE
; FILE REFERENCE: 10287/031001
; CURRENT APPLICATION NUMBER: US/09/019,348
; CURRENT FILING DATE: 1998-02-05
; EARLIER APPLICATION NUMBER: US 08/733,622
; EARLIER FILING DATE: 1996-10-17
; EARLIER APPLICATION NUMBER: US 60/017,646
; EARLIER FILING DATE: 1996-05-14
; EARLIER APPLICATION NUMBER: US 60/005,527
; EARLIER FILING DATE: 1995-10-18
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-019-348-25

alignment_scores:
Quality: 2467.00 Length: 461
Ratio: 5.351 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-08-711-417C-165 x US-09-019-348-25 ..
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216 AATGAATGGGGAAGAATGTCCGGAGGATTTACGAATGCTTGATGCTCGG 265
|||||
17 uMetAsnGlyGluCysAlaGluAspLeuArgMetLeuAspAlaSerG 34
266 GAGAGAAATGAATGGCTCCACAGGACCAAGGACGCTCGGCTTTGTGC 315
|||||
34 lyGluLysMetAsnGlySerHisArgAspGlnGlySerSerAlaLeuSer 50
316 GGAGTTGGAGGCATTCGACTTCCTTAACGGAAACTAAAGTGTGATATCTG 365
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51 GlyValGlyGlyIleArgLeuProAsnGlyLysLeuLysCysAspIleCy 67
366 TGGGATCATTTGCATCGGCCCAATGCTCATGTTTCACAAAGAAGCC 415
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67 sGlyIleCysIleGlyProAsnValLeuMetValHisLysArgSerH 84
416 ACATGGAGAACGGCCCTTCCAGTGAATCAGTGCAGGCGGCGCTCATTCAC 465
|||||
84 isThrGlyGluArgProPheGlnCysAsnGlnCysGlyAlaSerPheThr 100
466 CAGAGGGCAACCTGCTCCGGCACATCAAGCTGCATTCCGGGGAGAGCC 515
|||||
101 GlnLysGlyAsnLeuLeuArgHisIleLysLeuHisSerGlyGluLysPr 117
516 CTTCAAATGCCACTCTGCAACTACGCTCCGCCCGGAGGAGCGCCCTCA 565
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117 oPheLysCysHisLeuCysAsnTyrAlaCysArgArgArgAlaLeuT 134
566 CTGCCACCTGAGGACGCGCTCGTTGGTAAACCTCACAAATGTGGATAT 615
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134 hrGlyHisLeuArgThrHisSerValGlyLysProHisLysCysGlyTyr 150
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666 CTGCCACAACACTTGGAAAGCATGGCTTCCGGGCACACTGTACCCAG 715
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167 gCysHisAsnTyrLeuGluSerMetGlyLeuProGlyThrLeuTyrProV 184
716 TCATTAAAGAAAGAACTAAGCACAGTGAATGGCAGAGACCTGTGCAAG 765
|||||
184 alileLysGluGluThrLysHisSerGluMetAlaGluAspLysCysLys 200
766 ATAGATCAGAGAGATCTCTCGTCTGGACAGACTAGCAAGTAAATGTCG 815
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201 IleGlySerGluArgSerLeuValLeuAspArgLeuAlaSerAsnValAl 217
816 CAACAGCTAAGAGCTCTATGCTCCAGAAATTTCTTGGGGCAAGGCTGT 865
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217 aLysArgLysSerSerMetProGlnLysPheLeuGlyAspLysGlyLeuS 234
866 CGGACACCCCTCAGACAGTGTCCAGTACGAGAGAGGAGAACGAAATGATG 915
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234 erAspThrProTyrAspSerAlaThrTyrGluLysGluAsnGluMetMet 250
916 AAGTCCACAGGTGAGACCAAGCCATCAACAGCCCATCACTACCTGGG 965
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251 LysSerHisValMetAspGlnAlaIleAsnAsnAlaIleAsnTyrLeuGl 267
966 GGCCGAGTCCCTGGCCGCTGTGTGAGACGCGCCGCGGCTTCGAGG 1015
267 yAlaGluSerLeuArgProLeuValGlnThrProGlyGlySerGluV 284
1016 TGTTCGCGGTCAACAGCCCGATGTACAGCTGCACAGGCGCTCGAGGGC 1065
284 alValProValIleSerProMetTyrGlnLeuHisArgArgSerGluGly 300
1066 ACCCGCGCTCCCAACCACTCGGCCAGGACGCGGCTGGAGTACTCTGCT 1115
301 ThrProArgSerAsnHisSerAlaGlnAspSerAlaValGluTyrLeuLe 317
1116 GCTGCTCTCCAGGCCAAGTGTGCTGCTCGGAGCGCGGAGCGTCCCGA 1165
317 uLeuLeuSerLysAlaLysLeuValProSerGluArgGluAlaSerProS 334
1166 GCAACAGCTGCCAAGACTCCACGGACACGAGAGCAACACAGGAGGAGC 1215
334 erAsnSerCysGlnAspSerThrAspThrGluSerAsnAsnGluGluGln 350
1216 CGCAGCGGTCTTATCTACTGTACCAACCAACATCGCCGACGCGGCAACG 1265
351 ArgSerGlyLeuIleTyrLeuThrAsnHisIleAlaArgArgAlaGlnAr 367
1266 CGTGTCTGCTCAAGGAGGAGCAGCGGCTTACGAGCTGCTCGCGCCGCT 1315
367 gValSerLeuLysGluGluHisArgAlaTyrAspLeuLeuArgAlaAla 384
1316 CCGAGAACTCCGAGACCGCTCGCGGTGTCAGCACACGCGGGAGCAG 1365
384 erGluAsnSerGlnAspAlaLeuArgValSerThrSerGlyGluGln 400
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401 MetLysValTyrLysCysGluHisCysArgValLeuPheLeuAspHisVa 417
1416 CATGTACACCATCCACATGGGCTGCCAGGCTTCCGTTGATCCTTTGAGT 1465
417 lMetTyrThrIleHisMetGlyCysHisGlyPheArgAspProPheGluC 434
1466 GCAACATGTGCGGTACACAGCAGGACCGGTACGAGTTCTGTCGTCGAC 1515
434 ysAsnMetCysGlyTyrHisSerGlnAspArgTyrGluPheSerSerHis 450

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451 lIleThrArgGlyGluHisArgPheHisMetSer 461

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seq_name: /cgn2_6/ptodata/2/paa/US090_COMB pep:US-09-019-348A-25

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seq_documentation_block:
: Sequence 25, Application US/09019348A
: GENERAL INFORMATION:
: APPLICANT: Georgopoulos, Katia
: APPLICANT: Morgan, Bruce A.
: TITLE OF INVENTION: AIOLOS GENE
: FILE REFERENCE: 10287-031001
: CURRENT APPLICATION NUMBER: US/09/019,348A
: CURRENT FILING DATE: 1998-02-05
: PRIOR APPLICATION NUMBER: US 08/733,622
: PRIOR FILING DATE: 1996-10-17
: PRIOR APPLICATION NUMBER: US 60/017,646
: PRIOR FILING DATE: 1996-05-14
: PRIOR APPLICATION NUMBER: US 60/005,529
: PRIOR FILING DATE: 1995-10-18
: NUMBER OF SEQ ID NOS: 38
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 25
: LENGTH: 461
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-019-348A-25

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alignment_scores:
Quality: 2467.00      Length: 461
Ratio: 5.351         Gaps: 0
Percent Similarity: 100.000      Percent Identity: 100.000

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alignment_block:

US-08-711-417C-165 x US-09-019-348A-25

Align seg 1/1 to: US-09-019-348A-25 from: 1 to: 461

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166 AATGTTAAAGTAGAGACTCAGAGTCATGAAGAGAAATGGCGTGTGTA 215
|||||
1 AsnValLysValGluThrGlnSerAspGluGluAsnGlyArgAlaCysGl 17
216 AATGAATGGGGAAGATGTGGGAGGATTTACGATGCTTGCCTCGG 265
|||||
17 uMetAsnGlyGluGluCysAlaGluAspLeuArgMetLeuAspAlaSerG 34
266 GAGAGAAATGAATGGCTCCACAGGGACCAAGGAGCTCGGCTTGTG 315
|||||
34 lyGluLysMetAsnGlySerHisArgAspGlnGlySerSerAlaLeuSer 50
316 GGAGTTGGAGGCAATTCGACTTCCTTAACGGAAACTAAAGTGTGATCTG 365
|||||
51 GlyValGlyGlyIleArgLeuProAsnGlyLysLeuLysCysAspIleCy 67
366 TGGGATCAATTTGCATCGGGCCCAATGTCTCATGTTCACAAAAGAGCC 415
|||||
67 sGlyIleIleCysIleGlyProAsnValLeuMetValHisLysArgSerH 84
416 ACATGTGAGAACGGCCCTTCCAGTGCATCAGTCCGGGCGCTCATTCACC 465
|||||
84 isThrGlyGluArgProPheGlnCysAsnGlnCysGlyAlaSerPheThr 100
466 CAGAAGGCAACCTGCTCCGGCACATCAAGCTGCTTCCGGGGAGAGCC 515
|||||
101 GlnLysGlyAsnLeuLeuArgHisIleLysLeuHisSerGlyGluLysEr 117
516 CTTCAATATGCACCTCTGCAACTACGCTGCGCGGAGGAGCGCCCTCA 565
|||||
117 oPheLysCysHisLeuCysAsnTyrAlaCysArgArgAspAlaLeuT 134

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us-08-711-417c-165.rapm

Wed Aug 28 10:05:37 2002

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566 CTGGCCACTGAGGACGACCTCCGTTGGTAAACCTCACAATGTGGATAT 615
134 hrGlyHisLeuArgThrHisSerValGlyLysProHisLysCysGlyTyr 150
616 TGTGGCCGAAGCTATAACAGCAGCAACGCTTTTAGAGGAACAATAAGAGCG 665
151 CysGlyArgSerTyrLysGlnArgThrSerLeuGluHisLysGluAr 167
666 CTGCCACAACACTACTTGGAAAGCATGGGCTTCCGGGCACACTGTACCCAG 715
167 gCysHisAsnTyrLeuGluSerMetGlyLeuProGlyThrLeuTyrProV 184
716 TCATTAAAGCAAGAACTAAGCAGCAGTGAATGGCAGAGACCTGTGCAAG 765
184 alileLysGluGluThrLysHisSerGluMetAlaGluAspLeuCysLys 200
766 ATAGGATCAGAGAGATCTCTGTGTGGACAGACTAGCAAGTATGTGCG 815
201 IleGlySerGluArgSerLeuValLeuAspArgLeuAlaSerAsnValAl 217
816 CAAACGTAAAGCTCTATGCTCAGAAATTTCTTGGGACAAAGGCCCTGT 865
217 aLysArgLysSerSerMetProGlnLysPheLeuGlyAspLysGlyLeuS 234
866 CCGACAGCCCTACGACAGTGCACCTAGCAGAGGAGAGAACCAATGATG 915
234 erAspThrProTyrAspSerAlaThrTyrGluLysGluAsnGluMetWet 250
916 AAGTCCACGCTGATGGACCAAGCCATCAACAGCCCATCACTACTGCGG 965
251 LysSerHisValMetAspGlnAlaIleAsnAsnAlaIleAsnTyrLeuGl 267
966 GCGCAGTCCCTGCGCCGCTGTGTCAGAGCCGCCCGCGGCTTCGAGG 1015
267 yAlaGluSerLeuArgProLeuValGlnThrProProGlyGlySerGluV 284
1016 TGGTCCCGGTCTACAGCCCGATGTACAGCTGCACAGGCGCTCGGAGGCG 1065
284 alValProValIleSerProMetTyrGlnLeuHisArgSerGluGly 300
1066 ACCCGCGCTCCAAACCTCGGCCAGGACAGCGCGCTGGAGTACCTGCT 1115
301 ThrProArgSerAsnHisSerAlaGlnAspSerAlaValGluTyrLeuLe 317
1116 GCTGCTCTCCAGGCCAAGTGTGGTCCCTCGGAGCGGAGGCGCTCCCGA 1165
317 uLeuLeuSerLysAlaLysLeuValProSerGluArgGluAlaSerProS 334
1166 GCAACAGCTGCCAAGACTCCACGACACCGAGACCAACAGAGGAGCAG 1215
334 erAsnSerCysGlnAspSerThrAspThrGluSerAsnGluGluGln 350
1216 CGCAGCGGTCTTATCTACTGACCAACACATCGCCGCGCGCGCAACG 1265
351 ArgSerGlyLeuIleTyrLeuThrAsnHisIleAlaArgArgAlaGlnAr 367
1266 CGTGTGCTCAAGGAGGAGCAGCGCGCTTACGACCTGTGCGCGCGCGCT 1315
367 gValSerLeuLysGluGluHisArgAlaTyrAspLeuLeuArgAlaAlaS 384
1316 CCGAGAACTCGCAGGACGCGCTCCCGGTGGTGCAGCACCAGCGGGAGCAG 1365
384 erGluAsnSerGlnAspAlaLeuArgValValSerThrSerGlyGluGln 400
1366 ATCAAGGTGTACAAGTGGCAACACTGCCGGGTGCTCTTCCTGGATCAGT 1415
401 MetLysValTyrLysCysGluHisCysArgValLeuPheLeuAspHisVa 417
1416 CATGTACACCATCCACATGGGTGCGCACCGGCTTCCGTGATCTTTTGAGT 1465
417 lMetTyrThrIleHisMetGlyCysHisGlyPheArgAspProPheGluC 434
1466 GCAACATGTGCGGCTACACAGCCAGCGGCTACGAGTCTCTCTCGCAC 1515
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434 yAsnMetCysGlyTyrHisSerGlnAspArgTyrGluPheSerSerHis 450

1516 ATAACGGGAGGAGCAGCAGCGCTCCACATGAGC 1548

451 lIleThrArgGlyGluHisArgPheHisMetSer 461

seq_name: /cgn2_6/ptodata/2/paa/US097_COMB.pep:US-09-755-830-38

seq_documentation_block:
; Sequence 38, Application US/09755830
; GENERAL INFORMATION:
; APPLICANT: Georgopoulos, Katia
; TITLE OF INVENTION: IKAROS REGULATORY ELEMENTS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 10287-067001
; CURRENT APPLICATION NUMBER: US/09/755,830
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 08/283,300
; PRIOR FILING DATE: 1994-07-29
; PRIOR APPLICATION NUMBER: US 08/238,212
; PRIOR FILING DATE: 1994-05-02
; PRIOR APPLICATION NUMBER: US 08/121,438
; PRIOR FILING DATE: 1993-09-14
; PRIOR APPLICATION NUMBER: US 07/946,233
; PRIOR FILING DATE: 1992-09-14
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 461
; TYPE: PRM
; ORGANISM: Homo sapiens
; US-09-755-830-38

alignment_scores:
Quality: 2467.00 Length: 461
Ratio: 5.351 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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1 AsnValLysValGluThrGlnSerAspGluGluAsnGlyArgAlaCysG 17
216 AATGAATGGGAAGAATGTCGGAGGATTTACGAATGCTTGATGCCCTCG 265
17 uMetAsnGlyGluGluCysAlaGluAspLeuArgMetLeuAspAlaSerG 34
266 GAGAGAAATGAATGGTCCCGACAGGACCAAGCAGCTCGGCTTTGTCG 315
34 lyGluLysMetAsnGlySerHisArgAspGlnGlySerSerAlaLeuSer 50
316 GGAGTTGGAGGCAATTCGACTTCCTTAACGGAATAAAGTGTGATATCTG 365
51 GlyValGlyGlyIleArgLeuProAsnGlyLysLeuLysCysAspIleCy 67
366 TGGGATCATTTGCTATCGGGCCCAATGTCTCATGTTTCACAAAAGAAGCC 415
67 sglyIleIleCysIleGlyProAsnValLeuMetValHisLysArgSerH 84
416 ACACCTGGAGAGCGGCTTCACAGTGCATCATCAGTCGGGGGCTCATTCACC 465
84 lIleThrGlyGluArgProPheGlnCysAsnGlnCysGlyAlaSerPheThr 100
466 CAGAAGGGCAACCTCTCTCGGACATCAAGCTGCTATTCGGGGGAGAGCC 515
101 GlnLysGlyAsnLeuArgHisIleLysLeuHisSerGlyGluLysPr 117

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516 CTTCAATGCCACTCTGCAACTACGCTGCCGCCGAGGAGCGCCCTCA 565
117 oPheLysCysHisLeuCysAsnTyrAlaCysArgArgAspAlaLeuT 134
566 CTGCCACCTTGAGCGCAGCTCGTGGTAAACCTCAAAATGTGGATAT 615
134 hrGlyHisLeuArgThrHisSerValGlyLysProHisLysCysGlyTyr 150
616 TGTGGCGGAAGCTATAAACAGCGAAGCTCTTTAGAGGAACATAAAGACG 665
151 CysGlyArgSerTyrLysGlnArgThrSerLeuGluHisLysGluAr 167
666 CTGCCAACTACTTGGAAAGCATGGCTTCCGGGACACACTGTACCCAG 715
167 gCysHisAsnTyrLeuGluSerMetGlyLeuProGlyThrLeuTyrProV 184
716 TCATTAAGAAGAACTAAGCACAGTGAATGGCAGAGACCTGTGCAAG 765
184 aLileLysGluGluThrLysHisSerGluMetAlaGluAspLeuLys 200
766 ATAGGATCAGAGAGATCTCTGCTGGACAGACTAGCAAGTAAATGTCG 815
201 lleGlySerGluArgSerLeuValLeuAspArgLeuAlaSerAsnValAl 217
816 CAAAGCTTAAGAGCTCTATGCTCTAGAATTTCTTGGGCAAGGCGCTGT 865
217 aLysArgLysSerSerMetProGlnLysPheLeuGlyAspLysGlyLeuS 234
866 CCGACACGCCCTACGACAGTGCACAGTACGAGAGGAGAGCAAAATGATG 915
234 erAspThrProTyrAspSerAlaThrTyrGluLysGluAsnGluMetMet 250
916 AAGTCCACGCTGATGGACCAAGCATCAACAACGCCATCAACTACTCTGG 965
251 LysSerHisValMetAspGlnAlaIleAsnAsnAlaIleAsnTyrLeuG 267
966 GGCGAGCTCCCTCGGCCGCTGTGTGAGAGCGCCCGGCGGTTCGAGG 1015
267 yAlaGluSerLeuArgProLeuValGlnThrProGlyGlySerGluV 284
1016 TGTGTCGGGTATCAGCCCGATGTACAGCTGCACAGCGCTCGGAGGC 1065
284 alValProValIleSerProMetTyrGlnLeuHisArgSerGluGly 300
1066 ACCCCGCGCTCAACACACTCCGCGCCAGACAGCGCGCTGGAGTACCTGCT 1115
301 ThrProArgSerAsnHisSerAlaGlnAspSerAlaValGluTyrLeuLe 317
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317 uLeuLeuSerLysAlaLysLeuValProSerGluArgGluAlaSerProS 334
1166 GCAACAGCTGCCAAGACTCCAGGACCCGAGACGCAACAGAGAGCAG 1215
334 erAsnSerCysGlnAspSerThrAspThrGluSerAsnAsnGluGln 350
1216 CGCAGCGCTCTATCTACTGACCAACACACATCCCGCGAGCGCGCAAG 1265
351 ArgSerGlyLeuIleTyrLeuThrAsnHisIleAlaArgArgAlaGlnAr 367
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367 gValSerLeuLysGluGluHisArgAlaTyrAspLeuLeuArgAlaAlaS 384
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384 erGluAsnSerGlnAspAlaLeuArgValValSerThrSerGlyGluGln 400
1366 ATGAAGTGTACAAAGTCCGAACACTGCCGGGTGCTCTTCTGTGATCACGCT 1415
401 MetLysValTyrLysCysGluHisCysArgValLeuPheLeuAspHisVa 417
1416 CATGTACACCATCCACATGGGCTGCCACGGCTTCCGTGATCCTTTTGAGT 1465

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|||||
417 lmetTyrThrIleHisMetGlyCysHisGlyPheArgAspProPheGluC 434
1466 GCAACATGTGGCGCTACACACAGCCAGGACCGGTACGAGTTCTCGTCGCAC 1515
434 yAsnMetCysGlyTyrHisSerGlnAspArgTyrGluPheSerSerHis 450
1516 ATAACCGAGGAGCAGCCGCTCCACATGAGC 1548
451 IleThrArgGlyGluHisArgPheHisMetSer 461

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seq_name: /cgn2_6/ptodata/2/paa/PTUS_COMB.pcp: PCT-US99-02559-27

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seq_documentation_block:
; Sequence 27, Application PC/TUS9902559
; GENERAL INFORMATION:
; APPLICANT: Shiseido Co., Ltd.
; TITLE OF INVENTION: AIOLOS GENE
; FILE REFERENCE: 10287/031W01
; CURRENT APPLICATION NUMBER: PCT/US99/02559
; EARLIER FILING DATE: 1999-02-05
; EARLIER FILING DATE: 1998-02-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US99-02559-27

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Ratio: 4.913 Gaps: 6
Percent Similarity: 95.202 Percent Identity: 89.635

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US-08-711-417C-165 x PCT-US99-02559-27 ..

Align seg 1/1 to: PCT-US99-02559-27 from: 1 to: 518

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51 CCCCCCTGTAAGCGATCTCCAGATGAGGGCGGATGAGCCCATGCCGATCC 100
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17 rProValSerAspThrProAspGluGlyAspGluProMetProValP 34
101 CCGAGGACCTCTCCACCCTCGGAGGACAGCAAAAGCTCAAGAGTGAC 150
|||||
34 roGluAspLeuSerThrThrSerGlyAlaGlnGlnAsnSerLysSerAsp 50
151 AGAGTCGTGGCCAGTAACTTAAAGTAGACTCAGAGTGTATGAAGAGAA 200
|||||
51 ArgGlyMetAlaSerAsnValLysValGluThrGlnSerAspGluGluas 67
201 TGGCGCTGCTCTGAAATGAATGGGGAAGAATGTGGGAGGATTTACGAA 250
|||||
67 nGlyArgAlaCysGluMetAsnGlyGluGluCysAlaGluAspLeuArg 84
251 TGCTTTGATGCTCGGAGAGAAATGAATGGCTCCACAGGACCAAGGC 300
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84 etLeuAspAlaSerGlyGluLysMetAsnGlySerHisArgAspGlnGly 100
301 AGCTCGGCTTTGTGGGAGTTGGAGGACTTCGACTTCCTTAACGGAAACT 350
|||||
101 SerSerAlaLeuSerGlyValGlyGlyIleArgLeuProAsnGlyLysLe 117
351 AAAGTGTGATATCTGTGGGATCATTTGTCATCGGCGCCCAATGTGCTCATGG 400
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117 uLysCysAspIleCysGlyIleValCysIleGlyProAsnValLeuMetV 134

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Wed Aug 28 10:05:37 2002

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401 TTCAAAAAGAGCCACACTGAGAACGGCCCTTCCAGTGCATCAATGCG 450
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451 GGGGCTCATTCACACAGAGGACCACTGCTCCGGCACATCAAGCTGCA 500
|||||
151 GlyAlaSerPheThrGlnLysGlyAsnLeuLeuArgHisIleLysLeuHi 167
|||||
501 TTCGGGAGAGCCCTTCAATGGCACCTCTGCAACTACGCTCCGCC 550
|||||
167 sSerGlyGluLysProPheLysCysHisLeuCysAsnTyrAlaCysArgA 184
|||||
551 GGAGGAGCCCTCACTGGCCCACTCAGACGACACTCCGCTTGGTAAACCT 600
|||||
184 rgArgAspAlaLeuThrGlyHisLeuArgThrHisSerValGlyLysPro 200
|||||
601 CACAAATGTGGATATTGTGGCCGAAGCTATAAACACGCAAGCTCTTGA 550
|||||
201 HisLysCysGlyTyrCysGlyArgSerTyrLysGlnArgSerSerLeuGl 217
|||||
651 GGAACATAAGAGCGCTGCCACAACTACTTGGAAAGCATGGGCTTCCGG 700
|||||
217 uGluHisLysGluArgCysHisAsnTyrLeuGluSerMetGlyLeuProG 234
|||||
701 GCACACTGTACCCAGTCAATTAAGAAGAACTAAGCACAGTGAATGGCA 750
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234 ly...ValCysProValIleLysGluGluThrAsnHisAsnGluMetAla 249
|||||
751 GAAGACCTGTGCAAGATAGGATCAGAGATCTCTCGTGGGACAGACT 800
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250 GluAspLeuLysLysIleGlyAlaGluArgSerLeuValLeuAspArgLe 266
|||||
801 ACCAAGTATGTCGCAACAGTAAAGCTCTATGCCTCAGAAATTTCTTG 850
|||||
266 uAlaSerAsnValAlaLysArgLysSerSerMetProGlnLysPheLeuG 283
|||||
851 GGGACAAGCGCTGTCGACAGCGCCCTACGACAGTCCACCTACGAGAAG 900
|||||
283 lyAspLysCysLeuSerAspMetProTyrAspSerAlaAsnTyrGluLys 299
|||||
901 GACAAGCAATGATGAAGTCCACAGCTGATGGACCAAGCCATCAACAAGC 950
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300 Glu...AspMetThrSerHisValMetAspGlnAlaIleAsnAla 315
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951 CATCAACTACTGGGGCGAGTCCCTGCGCGCTGTGTGACAGCGCCC 1000
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315 alleAsnTyrLeuGlyAlaGluSerLeuArgProLeuValGlnThrProp 332
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1001 CGGCGGTTCCGAGGTGGTCCCGGTCTATCAGCCCGATGTACAGCTGCAC 1050
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332 roGlySerSerGluValValProValIleSerSerMetTyrGlnLeuHis 348
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1051 AGG...CGCTCGAGGCGACCCCGCTCCACCACTCGCGCCGACAGACAG 1097
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349 LysProProSerAspGlyProProArgSerAsnHisSerAlaGlnAsp... 364
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398 SerAsnAlaGluGluGlnArgSerGlyLeuIleTyrLeuThrAsnHisI 414
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1295 AGCACTGCTGCGCGCCCTCCGAGAACTCGCAGGACGCGCTCCGCGTG 1344
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431 yzGluValLeuLeuArgAlaAlaSerGluAsnSerGlnAspAlaPheArgVal 447
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|||||
448 ValSerThrSerGlyGluGlnLeuLysValTyrLysCysGluHisCysAr 464
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1395 GGTGCTCTCTCTGATCAGCTCATGTACACCATCCACATG.....G 1435
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481 lyCysHisGlyPheArgAspProPheGluCysAsnMetCysGlyTyrHis 497
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; Sequence 27, Application US/09019348
; GENERAL INFORMATION:
; APPLICANT: Georgopoulos, Katia
; APPLICANT: Morgan, Bruce
; TITLE OF INVENTION: AJOLOX GENE
; FILE REFERENCE: 10287/031001
; CURRENT APPLICATION NUMBER: US/09/019, 348
; EARLIER FILING DATE: 1998-02-05
; EARLIER APPLICATION NUMBER: US 08/733,622
; EARLIER FILING DATE: 1996-10-17
; EARLIER APPLICATION NUMBER: US 60/017,646
; EARLIER FILING DATE: 1996-05-14
; EARLIER APPLICATION NUMBER: US 60/005,527
; EARLIER FILING DATE: 1995-10-18
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-019-348-27
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Ratio: 4.913 Gaps: 6
Percent Similarity: 95.202 Percent Identity: 89.635
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1 MetAspValAspGluGlyGlnAspMetSerGlnValSerGlyLysGluSe 17
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51 CCCCCCTGTAAAGCGATCTCCAGATGAGGCGGATGAGCCATGCCGATCC 100
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17 rProProValSerAspThrProAspGluGlyAspGluProMetProValp 34
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101 CCGAGGACCTCTCCACCACCTCCGGGAGGACAGCAAGCTCCAAAGAGTGAC 150
|||||
34 roGluAspLeuSerThrThrSerGlyAlaGlnGlnAsnSerLysSerAsp 50
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151 AGAGTCGTGGCCAGTAAATGTTAAAGTAGAGACTCAGAGTGTATGAAGAA 200
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alignment_block:

US-08-711-417C-165 x US-09-019-348A-27 ..

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51 CCCCCCTGTAAGGATACCTCCAGATCAGGCGCATGAGCCCATGCCATCC 100
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17 rProValSerAspThrProAspGluGlyAspGluProMetProValP 34
101 CCGAGGACCTCTCCACACCTCGGAGGACAGCAAGCTCCAAGAGTGAC 150
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34 roGluAspLeuSerThrSerGlyAlaGlnGlnAsnSerLysSerAsp 50
151 AGAGTCGTGGCCAGTAATGTTAAAGTAGAGACTCAGAGTGATGAGAGAA 200
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51 ArgGlyMetAlaSerAsnValLysValGluThrGlnSerAspGluGluAs 67
201 TGGCGCTGCTGTGAATGAATGGGGAAGAATGTGCGGAGGATTACGAA 250
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251 TGCTTGATGCCTCGGAGAGAAATGAATGGCTCCACAGGACCAAGGC 300
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301 AGTCGGCTTTGTCGGGAGTTGGAGCATTCGACTTCCTAACGGAAACT 350
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101 SerSerAlaLeuSerGlyValGlyGlyIleArgLeuProAsnGlyLysLe 117
351 AAAGTCGTATATCTGGGATCATTTGGCATCGGCCCAATGTGCTCATGG 400
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117 uLysCysAspIleCysGlyIleValCysIleGlyProAsnValLeuMetV 134
401 TTCACAAAAGAACCCACTGGAGAACGGCCCTTCAGTGCAATCAGTGC 450
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151 GlyAlaSerPheThrGlnLysGlyAsnLeuLeuArgHisIleLysLeuHi 167
501 TTCGGGGAGAACCCCTTCAATGCCACCTCTGCAACTACGCTCGCGCC 550
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167 sSerGlyGluLysProPheLysCysHisLeuLysCysAsnTyrAlaCysArgA 184
551 GGAGGACGCCCTCACTGGCCACCTGAGGACGCACTCCGTTGGTAAACT 600
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184 rArgAspAlaLeuThrGlyHisLeuArgThrHisSerValGlyLysPro 200
601 CACAAATGTGGATATTGCGCGAGGCTATAACAGCGCACTCTTTAGA 650
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217 uGluHisLysGluArgCysHisAsnTyrLeuGluSerMetGlyLeuProG 234
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250 GluAspLeuCysLysIleGlyAlaGluArgSerLeuValLeuAspArgLe 266
801 AGCAAGTAATGTCGCAAAACGTAAGAGCTCTATGCTCAGAAATTTCTTG 850
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266 uAlaSerAsnValAlaLysArgLysSerSerMetProGlnLysPheLeuG 283

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851 GGGACAAAGGGCTGTCCGACACAGCCCTTACAGACTGCCAGCTAGCAGAG 900
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283 lyAspLysCysLeuSerAspMetProTyrAspSerAlaAsnTyrGluLys 299
901 GAGAACGAATGATGAAGTCCACGTGATGGACCAAGCCATCAACAACGC 950
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951 CATCAACTACCTGGGGCGGAGTCCCTCGCGCTGCTGGTGCAGACGCC 1000
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315 alIeAsnTyrLeuGlyAlaGluSerLeuArgProLeuValGlnThrProp 332
1001 CGGCGGTTCCGAGGTGCTCCCGGTATCATGACCCGATGTACCACTGCAC 1050
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332 roGlySerSerGluValValProValIleSerSerMetTyrGlnLeuHis 348
1051 AGG...CGCTCGGAGGGACCCCGCTCCAACCACTCGGCCCGAGGACAG 1097
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349 LysProProSerAspGlyProProArgSerAsnHisSerAlaGlnAsp.. 364
1098 CGCGGTGGAGTACCTGCTGCTCTCTCAAGGCCAAGTTGGTGCCTCGG 1147
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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381 luArgGluAlaSerProSerAsnSerCysGlnAspSerThrAspThrGlu 397
1198 AGCAACAACGAGGAGCAGCGCGGTCTTATCTACCTGACCAACACCAT 1247
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398 SerAsnAlaGluGluGlnArgSerGlyLeuIleTyrLeuThrAsnHisII 414
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414 eAsnProHisAlaArgAsnGlyLeuAlaLeuLysGluGluArgAlaT 431
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1395 GGTGCTCTTCTGGATCAGTCATGTACACCATCCACATG.....G 1435
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481 lyCysHisGlyPheArgAspProPheGluCysAsnMetCysGlyTyrHis 497
1486 AGCCAGGACCGGTACGAGTTCTGTCGCACATAACGCGAGGGAGCAGCG 1535
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1536 CTTCACATGAGC 1548
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514 gTyrHisLeuSer 518

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seq_name: /cqn2_6/ptodata/2/paa/US097_COMB.pep:US-09-755-830-40

seq_documentation_block:

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; Sequence 40, Application US/09755830
; GENERAL INFORMATION:
; APPLICANT: Georgopoulos, Katia
; TITLE OF INVENTION: IKAROS REGULATORY ELEMENTS AND USES
; FILE REFERENCE: 10287-067001
; CURRENT APPLICATION NUMBER: US/09/755,830
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 08/283,300
; PRIOR FILING DATE: 1994-07-29

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; PRIOR APPLICATION NUMBER: US 08/238,212
 ; PRIOR FILING DATE: 1994-05-02
 ; PRIOR APPLICATION NUMBER: US 08/121,438
 ; PRIOR FILING DATE: 1993-09-14
 ; PRIOR APPLICATION NUMBER: US 07/946,233
 ; PRIOR FILING DATE: 1992-09-14
 ; NUMBER OF SEQ ID NOS: 43
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 40
 ; LENGTH: 518
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; US-09-755-830-40

alignment_scores:
 Quality: 2437.00 Length: 521
 Ratio: 4.913 Gaps: 6
 Percent Similarity: 95.202 Percent Identity: 89.635

alignment_block:

US-08-711-417C-165 x US-09-755-830-40 ..

Align seg 1/1 to: US-09-755-830-40 from: 1 to: 518

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1 ATGGATGCTGACGAGGCTCAAGACATGCTCTTCTCATCAGGGAAGAAAG 50
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1 MetAspValaspGluGlnaspMetSerGlnValSerGlyLysGluSe 17
51 CCCCCCTGAAGGATACCTCAGATGAGGGCGATGAGCCCATGCCGATCC 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17 rProProValSerAspThrProAspGluGlyAspGluProMetProValP 34
101 CCAGGACCTCTCCACCACTCGGGAGGACAGCAAGCTCCAAGATGAC 150
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
34 roGluaspLeuSerThrSerGlyAlaGlnGlnAsnSerLysSerasp 50
151 AGAGTCGTGGCCAGTAAATGTAAGTAGAGACTCAGAGTGATCAAGAGAA 200
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
51 ArgGlyMetAlaSerAsnValLysValGluThrGlnSerAspGluGluAs 67
201 TGGCGTGCCTGTGAATGAATGGGGAAGAAATGTCGGGAGGATTTACGAA 250
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
67 nGlyArgAlaCysGluMetAsnGlyGluGluCysAlaGluAspLeuArgM 84
251 TGCTTGATGCTCGGAGAGAAATGAATGGCTCCACAGGGACCAAGGC 300
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
84 etLeuaspAlaSerGlyGluLysMetAsnGlySerHisargaspGlnGly 100
301 AGCTCGGCTTTGTCGGAGTTGGAGCATTCGACTTCCTTAACGGAAACT 350
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
101 SerSerAlaLeuSerGlyValGlyGlyIleArgLeuProAsnGlyLysLe 117
351 AAAGTGATATCTGGGATCATTTGCACTCGGGCCCAATGTCTCATGG 400
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
117 uLysCysaspIlecysglyIleValCysIleGlyProasnValLeuMetV 134
401 TTCACAAAAGAACCACTGGAGACGGCCCTTCCAGTGCAATCATGTC 450
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
134 alHisLysArgSerHisThrGlyGluArgProPheGlnCysAsnGlnSer 150
451 GGGGCTCATTCACCCAGAGGGCAACCTGCTCCGGCACATCAAGCTGCA 500
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
151 GlyAlaSerPheThrGlnLysGlyAsnLeuLeuArgHisIleLysLeuHi 167
501 TTCGGGGAGAGCCCTTCAATGCCACCTCTCAACTACGCTCGCGCC 550
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
167 sSerGlyGlnLysProPheLysCysHisLeuCysAsnThrAlaCysArgA 184
551 GGAGGGAGCCCTCACATGGCCACCTGAGGACGCACTCCGTTGGTAAACCT 600
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
184 rGargaspAlaLeuThrGlyHisLeuArgThrHisSerValGlyLysPro 200

```

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601 CACAAATGTGGATATTGTGGCCGAAGCTATAAACACGACGACGCTTTAGA 650
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
201 HisLysCysglyTyrCysGlyArgSerTyrLysGlnArgSerSerLeuG 217
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
651 GGAACATAAGAGCGCTGCCACAACTACTTGGAAAGCATGGGCTTCCGG 700
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
217 uGluHisLysGluArgCysHisAsnTyrLeuGluSerMetGlyLeuProG 234
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
701 GCACACTGTACCAGTCATTAAAGAACTAAGCACAGTGAATGGCA 750
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
234 ly...ValCysProValIleLysGluThrAsnHisAsnGluMetAla 249
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
751 GAAGACCTGTGCAAGATAGATCAGACAGATCTCTGCTGCTGCACAGACT 800
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
250 GluAspLeuCysLysIleGlyAlaGluArgSerLeuValLeuAspArgLe 266
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
801 AGCAAGTAATGTGCCAAACGTAAGAGCTCTATGCTCTCAGAAAATTTCTG 850
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
266 uAlaSerAsnValAlaLysArgLysSerSerMetProGlnLysPheLeuG 283
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
851 GGGACAAAGGCCCTGTCCGACACGCCCTTACGACAGTGCACGTACGAGAAG 900
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283 lyAspLysCysLeuSerAspMetProTyrAspSerAlaAsnTyrGluLys 299
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
901 GAGAACAAATGATGAAGTCCCAGCTGATGACCAAGCCCATCAACACGC 950
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300 Glu...AspMetMetThrSerHisValMetaspGlnAlaIleAsnAla 315
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
951 CATCAACTACCTGGGGCCGAGTCCCTGCGCCGCTGGTGCGACAGCCCC 1000
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
315 alLeasnTyrLeuGlyAlaGluSerLeuArgProLeuValGlnThrProp 332
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1001 CGGCGGTTCCGAGGTGTCGGTCTATCAGCCCGCTGATGATGATGATGATG 1050
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
332 roGlySerSerGluValValProValIleSerSerMetTyrGlnLeuHis 348
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1051 AGG...CGCTCGAGGACCCCGCTGCCAACTCCAGCCAGGACAG 1097
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
349 LysProSerAspGlyProProArgSerAsnHisSerAlaGlnAsp... 364
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1098 CGCGTGGAGTACCTGCTGCTCTCCAAGGCCAAGTTGGTGCCCTCGG 1147
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365 .AlaValAspAsnLeuLeuSerLysAlaLysSerValSerSerG 381
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1148 AGCGGAGGCGTCCCGAGCACAGCTCCCAAGACTCCACGACACCCGAG 1197
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
381 luArgGluAlaSerProSerAsnSerCysGlnAspSerThrAspThrGlu 397
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398 SerAsnAlaGluGluArgSerGlyLeuIleTyrLeuThrAsnHisIl 414
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|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
414 eAsnProHisAlaArgAsnGlyLeuAlaLeuLysGluGluArgAlaLat 431
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1295 AGGACCTGCTCGCGCCGCTCCGAGAACTCGCAGGACGCTCGCGCTG 1344
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431 yrGluValLeuArgAlaAlaSerGluAsnSerGlnAspAlaPheArgVal 447
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1345 GTCAGCACACGCGGGAGCAGATGAAGTGTACAACTCGCAACACTGCGG 1394
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
448 ValSerThrSerGlyGluGlnLeuLysValTyrLysCysGluHisCysAr 464
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1395 GTGTCTCTTCTGGATCAGCTCATGTACACCATCCACATG.....G 1435
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
464 gValLeuPheLeuAspHisValMetTyrThrIleHisMetGlyCysHisG 481
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
481 lycyshisGlyPheargaspProPheGluCysAsnMetCysGlyTyrHis 497
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1486 AGCCAGGACCGGTACGAGTTCTCTGTCGCACATAACGCGAGGGGACCG 1535

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498 SerGlnAspArgTyrGluPheSerHisIleThrArgGlyGluHisAr 514
 1536 CTTCCACATGAGC 1548
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seq_name: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pcp: PCT-US99-04224-7

seq_documentation_block:

; Sequence 7, Application PC/TUS9904224A
 ; GENERAL INFORMATION:
 ; APPLICANT: The General Hospital Corporation
 ; TITLE OF INVENTION: THE HELIOS GENE
 ; FILE REFERENCE: 10287/043W01
 ; CURRENT APPLICATION NUMBER: PCT/US99/04224A
 ; CURRENT FILING DATE: 1999-02-26
 ; EARLIER APPLICATION NUMBER: US 60/076,325
 ; EARLIER FILING DATE: 1998-02-27
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 7
 ; LENGTH: 517
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; PCT-US99-04224-7

alignment_scores:

Quality: 2426.50 Length: 521
 Ratio: 4.892 Gaps: 7
 Percent Similarity: 95.202 Percent Identity: 89.443

alignment_block:

US-08-711-417C-165 x PCT-US99-04224-7

Align seg 1/1 to: PCT-US99-04224-7 from: 1 to: 517

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 51 CCCCCCTGTAAAGCATCTCCACATGAGGGCGATGAGCCCATCCGATCC 100
 17 rProProValSerAspThrProAspGluGlyAspGluProMetProValp 34
 101 CCGAGGACCTCTCCACACCTCCGAGGAGCAGCAAAAGCTCCAGAGTGAC 150
 34 roGluAspLeuSerThrThrSerGlyAlaGlnGlnAsnSerLysSerAsp 50
 151 AGAGTCGTGCGCCAGTAATGTTAACTAGAGACTCAGAGTGAAGAGAA 200
 51 ArgGlyMetGlySerAsnValLysValGluThrGlnSerAspGluGluAs 67
 201 TGGGCGTCTGCTGAAATGAATGGGAAGAATGTGGGAGGATTTACGAA 250
 67 nGlyArgAlaCysGluMetAsnGlyGluGluCysAlaGluAspLeuArgW 84
 251 TGCTTGATGCTCGGAGAGAAATGAATGGTCCACAGGACCAAGGC 300
 84 etLeuAspAlaSerGlyGluLysMetAsnGlySerHisArgAspGlnGly 100
 301 AGCTCGGCTTGTGCGGAGTTGGAGGCATTCGACTTCCTAACGGAAACT 350
 101 SerSerAlaLeuSerGlyValGlyGlyIleArgLeuProAsnGlyLysLe 117
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 501 TTCGGGGAGAGCCCTTCAAAATGCCACCTCTGCAACTACGCTGCGCGC 550
 166 sSerGlyGluLysProPheLysCysHisLeuCysAsnTyrAlaCysArgA 183
 551 GGAGGACGCCCTCACTGCCCACCTGAGGACGCACTCCCTTGGTAAACCT 600
 183 rgArgAspAlaLeuThrGlyHisLeuArgThrHisSerValGlyLysPro 199
 601 CACAAATGTGGATATTGTGCCGCAAGCTATAAACAGCAGACGCTCTTAGA 650
 200 HisLysCysGlyTyrCysGlyArgSerTyrLysGlnArgSerSerLeuG 216
 651 GGAACATAAAGAGCGCTGCCACAACTACTTTGAAAGCATGGCCCTTCCGG 700
 216 uGluHisLysGluArgCysHisAsnTyrLeuGluSerMetGlyLeuProG 233
 701 GCACACTGTACCCAGTCATTAAAGAAGAACTAACACAGTGAATGGCA 750
 233 ly...ValCysProValIleLysGluGluThrAsnHisAsnGluMetAla 248
 751 GAAGACCTGTGCAAGATAGGATCAGAGATCTCTCGTCTGGACAGACT 800
 249 GluAspLeuCysLysIleGlyAlaGluArgSerLeuValLeuAspArg 265
 801 AGCAAGTAATGTGCCAAACGTAAGAGCTCTATGCTCAGAAATTTCTTG 850
 265 uAlaSerAsnValAlaLysArgLysSerSerMetProGlnLysPheLeuG 282
 851 GGGACAAGGGCTGTCGACACGCGCTACGACAGTCCACGCTACGAGAG 900
 282 lyAspLysCysLeuSerAspMetProTyrAspSerAlaAsnTyrGlnLys 298
 901 GAGAACGAAATGATGAGTCCCACGTGATGGACCAAGCCATCAACAAGC 950
 299 Glu...AspMetMetThrSerHisValMetAspGlnAlaIleAsnAsnAl 314
 951 CATCAACTACCTGGGGCGGAGTCCCTCGCGCCGCTGGTCAGACGCGCC 1000
 314 alLeuAsnTyrLeuGlyAlaGluSerLeuArgProLeuValGlnThrProp 331
 1001 CGGGCGTTCGAGGTGTCGCGGTCTATCAGCCGCGATGTACCCAGCTGCAC 1050
 331 roGlySerSerGluValValProValIleSerSerMetTyrGlnLeuHis 347
 1051 AGG...CGCTCGAGGGCACCCCGCTCCCAACCACTCGGCCAGGACAG 1097
 348 LysProProSerAspGlyProProArgSerAsnHisSerAlaGlnAsp... 363
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 364 AlaValAspAsnLeuLeuLeuSerLysAlaLysSerValSerSerG 380
 1148 AGCGGAGGCGTCCCGGAGCAACAGCTGCCAAGACTCCACGACACACGAG 1197
 380 luArgGluAlaSerProSerAsnSerCysGlnAspSerThrAspThrGlu 396
 1198 AGCAACACGAGGAGCAGCGCGGTCTTATCTACCTGACCAACACACAT 1247
 397 SerAsnAlaGluGluGlnArgSerGlyLeuIleTyrLeuThrAsnHisI 413
 1248 CGCCCCGAGCGCGCAACGC...GTGTCGCTCAAGGAGGACACCGCGCT 1294
 413 eAsnProHisAlaArgAsnGlyLeuAlaLeuLysGluGlnArgAlar 430
 1295 ACAGCTGCTCGCGCGCGCTCCGAGAACTCGCAGGACGCGCTCCGCGTG 1344
 430 yrGluValLeuArgAlaAlaSerGluAsnSerGlnAspAlaPheArgVal 446

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1345 GTCAGCACCGGGAGGAGCAGATGAAGTGTACAAAGTGCAGAACTGCCG 1394
|||||
447 ValSerThrSerGlyGluGlnLeuLysValTyrLysCysGluHisCysAr 463
1395 GGTGCTCTTCCTGGATCAGCTCATGTATACACATCCACATG.....G 1435
|||||
463 gValLeuPheLeuAspHisValMetTyrThrIleHisMetGlyCysHisG 480
1436 GCTGCCAGCGGCTTCGGTGCATCTCTTCAGTGCACATGTGGGTACAC 1485
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480 lYcysHisGlyPheArgAspProPheGluCysAsnMetCysGlyTyrHis 496
1486 AGCCAGGACCGGTACGAGTCTCTCGCACATAACGGGAGGGAGCACCG 1535
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497 SerGlnAspArgTyrGluPheSerSerHisIleThrArgGlyGluHisAr 513
1536 CTTCACATGAGC 1548
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seq_name: /cgn2_6/ptodata/2/paa/US092_COMB.pap.us-09-259-389-7

seq_documentation_block:
; Sequence 7, Application US/09259389
; GENERAL INFORMATION:
; APPLICANT: Georgopoulos, Katia
; APPLICANT: Morgan, Bruce A.
; APPLICANT: Kelly, Clair
; TITLE OF INVENTION: THE HELIOS GENE
; FILE REFERENCE: 10287/043001
; CURRENT APPLICATION NUMBER: US/09/259,389
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: US 60/076,325
; EARLIER FILING DATE: 1998-02-27
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-259-389-7
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alignment_scores:
  Quality: 2426.50      Length: 521
  Ratio: 4.892          Gaps: 7
Percent Similarity: 95.202 Percent Identity: 89.443
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alignment_block:

US-08-711-417c-165 x US-09-259-389-7 ..

Align seg 1/1 to: US-09-259-389-7 from: 1 to: 517

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1 MetAspValAspGluGlnAspMetSerGlnValSerGlyLysGluSe 17
51 CCCCCCTGTAAGCGATACCTCAAGATGAGGGCGATGAGCCCATGCCATCC 100
|||||
17 rProProValSerAspThrProAspGluGlyAspGluProMetProValP 34
101 CCAGGACCTCTCCACCTCGGGAGGACAGCAAGCTCCAGAGTGAC 150
|||||
34 roGluAspLeuSerThrThrSerGlyAlaGlnGlnAsnSerLysSerAsp 50
151 AGAGTCTGTGCCAGTAAATGTTAAAGTAGAGACTCAGAGTGCAGAGAA 200
|||||
51 ArgGlyMetGlySerAsnValLysValGluThrGlnSerAspGluGluAs 67
201 TGGCGCTGCTGTCAATGAATGCGGAAGAAATGTCGGGAGGATTTACGAA 250
|||||
67 nGlyArgAlaCysGluMetAsnGlyGluGluCysAlaGluAspLeuArgM 84
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251 TGTCTGATCCTCGGAGAGAAAATGAATGGCTCCACAGGACCAAGGC 300
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84 etLeuAspAlaSerGlyGluLysMetAsnGlySerHisArgAspGlnGly 100
301 AGCTCGGCTTTCGGGAGTTCGAGGCAATTCGACTTCCTTAACGGAAACT 350
|||||
101 SerSerAlaLeuSerGlyValGlyGlyIleArgLeuProAsnGlyLysLe 117
351 AAAGTCTGATATCTGTGGATCATTTTCATCGGGCCCAATGTGCTCATGG 400
|||||
117 uLysCysAspIleCysGlyIleValCysIleGlyProAsnValLeuMetV 134
401 TTCACAAAAGAACCCACACTGGAGAGCGCCCTTCAGTGCATCATGTCG 450
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134 alHisLysArgSerHisThr...GluArgProPheGlnCysAsnGlnCys 149
451 GGGGCTCTATTACCCAGAGGCAACCTGTCTCCGGCAGATCAAGCTGCA 500
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501 TTCGGGGAGAGCCCTTCAATGCCACCTCTGCAACTACGCTGCCGCC 550
|||||
166 sSerGlyGluLysProPheLysCysHisLeuCysAsnTyrAlaCysArgA 183
551 GGAGGAGCGCCCTCACTGGCCCACTGAGGACGCACTCCGTGTGTAACCT 600
|||||
183 rgArgAspAlaLeuThrGlyHisLeuArgThrHisSerValGlyLysPro 199
601 CACAAATCTGGATATTGTGGCCGAAGCTATAAACAGCAGCACTTTTAGA 650
|||||
200 HisLysCysGlyTyrCysGlyArgSerTyrLysGlnArgSerSerLeuG 216
651 GGAACATAAAGAGCGCTGCCAACAACACTACTTGGAAAGCATGGGCTTCC 700
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701 GCACACTGTACCCAGTCATTAAAGAGAACTAAGCACAGTGAATGGCA 750
|||||
233 ly...ValCysProValIleLysGluThrAsnHisAsnGluMetAla 248
751 GAAGACCTGTGCAAGATAGGATCAGAGATCTCTCGTGTGGACAGACT 800
|||||
249 GluAspLeuCysLysIleGlyAlaGluArgSerLeuValLeuAspArgLe 265
801 AGCAAGTAATGTCGCCAAAGCTAAGAGCTCTATGCTCAGAAATTTCTTG 850
|||||
265 uAlaSerAsnValAlaLysArgLysSerSerMetProGlnLysPheLeuG 282
851 GGGACAAAGGGCTGTCCGACACGCGCTTACGACAGTGCACGTACGAGAAG 900
|||||
282 lYAspLysCysLysLeuSerAspMetProTyrAspSerAlaAsnTyrGluLys 298
901 GAGAACGAATGATGAAGTCCCGCTGATGGACCAAGCCATCAACACGC 950
|||||
299 Glu...AspMetMetThrSerHisValMetAspGlnAlaIleAsnAl 314
951 CATCAACTACCTGGGGCGGAGTCCCTCGCGCCGCTGTGTGAGACGCCCC 1000
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314 alleAsnTyrLeuGlyAlaGluSerLeuArgProLeuValGlnThrProp 331
1001 CGGGCGGTTCGAGGTGTCCTGCTCATCAGCCCGATGTACCACTGCAC 1050
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331 roGlySerSerGluValValProValIleSerSerMetTyrGlnLeuHis 347
1051 AGG...CGCTCGGAGGACCCCGCTCCCAACCACTCGGCCAGGACAG 1097
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348 LysProProSerAspGlyProProArgSerAsnHisSerAlaGlnAsp.. 363
1098 CGCGCTGGAGTACCTGTCTGCTCTCCAAAGCCCAAGTGTGTCCTCGG 1147
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-121-438-5

alignment_scores:
    Quality: 2422.00      Length: 571
    Ratio: 4.863         Gaps: 7
    Percent Similarity: 87.215    Percent Identity: 82.137

alignment_block:
US-08-711-417C-165 x US-08-121-438-5  ..

Align seg 1/1 to: US-08-121-438-5 from: 1 to: 568

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1  MetAspValAspGluGlyGlnAspMetSerGlnValSerGlyLysGlu 17
51  CCCCCTGTGAAGGATACCTCCAGATCAGGCGCATGAGCCATGCCCATCC 100
17  rProProValSerAspThrProAspGluGlyAspGluProMetProVal 34
101 CCGAGGACCTCTCCACCACCTCGGGAGGACGAAAGCTCCCAAGAGTGC 150
34  roGluAspLeuSerThrThrSerGlyAlaGlnAsnSerLysSerAsp 50
151 AGAGTCGTGCGCCAGTAAATGTTAAAGTAGACATCAGATGCATCAAGAA 200
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51  ArgGlyMetAlaSerAsnValLysValGluThrGlnSerAspGluGlu 67
201 TGGCGCTGCTGTCAATGAATGGGAAGAATGTGCGGAGGATTTACGAA 250
67  nGlyArgAlaCysGluMetAsnGlyGluGluCysAlaGluAspLeuArg 84
251 TGCTTGATGCTCGGAGAGAAAATGAATGGTCCCCACAGGACCAAGCC 300
84  etLeuAspAlaSerGlyGlyLysMetAsnGlySerHisArgAspGlnGly 100
300 ..... 300

101 SerSerAlaLeuSerGlyValGlyGlyIleArgLeuProAsnGlyLysLe 117
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117 uLysCysAspIleCysGlyIleValCysIleGlyProAsnValLeuMetV 134
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151 SerSerAlaLeuSerGlyValGlyGlyIleArgLeuProAsnGlyLysLe 167
351 AAAGTCTGATATCTGGGATCATTTGCATCGGGCCCAATGTGCTCATGG 400
167 uLysCysAspIleCysGlyIleValCysIleGlyProAsnValLeuMetV 184
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251 HisLysCysGlyTyrCysGlyArgSerTyrLysGlnArgSerSerLeuG1 267
651 GGRACATAAGAGCGCTGCCACAACACTACTTGGAAAGCATGGCCCTCCGG 700
267 uGluHisLysGluArgCysHisAsnTyrLeuGluSerMetGlyLeuProG 284
701 GCACACTGTACCCAGTCATTAAAGAGAACTAAGCACACAGTGAATGCCA 750
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300 GluAspLysCysLysIleGlyAlaGluArgSerLeuValLeuAspArgLe 316
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seq_documentation_block:

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; Sequence 22, Application PC/TUS9902559
; GENERAL INFORMATION:
; APPLICANT: Shiseido Co., Ltd.
; TITLE OF INVENTION: AIOLOS GENE
; FILE REFERENCE: 10287/031W01
; CURRENT APPLICATION NUMBER: PCT/US99/02559
; CURRENT FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: US 09/019,348
; EARLIER FILING DATE: 1998-02-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(470)
; OTHER INFORMATION: xaa = Any Amino Acid
PCT-US99-02559-22

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alignment_scores:

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Quality: 2207.50      Length: 468
Ratio: 5.098          Gaps: 3
Percent Similarity: 92.521 Percent Identity: 90.385

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; Sequence 153, Application US/08465590B
; Patent No. 5777072
; GENERAL INFORMATION:
; APPLICANT: Georgopoulos, Katia A.
; TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
; NUMBER OF SEQUENCES: 191
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; CITY: BOSTON
; STREET: 28 STATE STREET, Suite 510
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Ascii (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,590B
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/238,212
; FILING DATE: 02-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/121,438

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Wed Aug 28 10:05:37 2002

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; FILING DATE: 14-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/946,233
; FILING DATE: 14-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Paul L. 35,695
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: MPG-006C2DV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 153:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 470 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: C-terminal
; US-08-465-590B-153

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  Ratio: 5.098          Gaps: 3
  Percent Similarity: 92.521  Percent Identity: 90.385

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; Sequence 22, Application US/08733622A
; GENERAL INFORMATION:
; APPLICANT: Katia Georgopoulos
; APPLICANT: Bruce Morgan
; TITLE OF INVENTION: The Aiolos Gene
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1775

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/733.622A
; FILING DATE: 17-OCT-1996

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/017,646
; FILING DATE: 14-MAY-1996

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,529
; FILING DATE: 18-OCT-1995

; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: MGP-042CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214

; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 470 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: peptide
; FRAGMENT TYPE: C-terminal
; US-08-733-622A-22

alignment_scores:

Quality: 2207.50 Length: 468
Ratio: 5.098 Gaps: 3
Percent Similarity: 92.521 Percent Identity: 90.385

alignment_block:

US-08-711-417c-165 x US-08-733-622A-22 ..

Align seg 1/1 to: US-08-733-622A-22 from: 1 to: 470

160 GCCAGTAATGTTAAAGTAGACTGAGATGATGAGAGAAATGGCGGTGC 209
|||||
3 AlaSerAsnValLysValGluThrGlnSerAspGluGluAsnGlyArgAl 19
210 CTGTGAATGAATGGGAAAGAAATGTCCGGAGGATTTACGAATGCTTGATG 259
|||||
19 acysGluMetAsnGlyGluGluCysAlaGluAspLeuArgMetLeuAsp 36
260 CTTCCGGAGAGAAATGAATGCTCTCCACAGGACCAAGGACGCTCGGCT 309
|||||
36 laSerGlyGluLysMetAsnGlySerHisArgAspGlnGlySerSerAla 52
310 TTGTCGGGAGTTGGAGGCATTCGACTTCTTAACGGAANAACCTAAAGTGTA 359

|||||
53 LeuSerGlyValGlyGlyIleArgLeuProAsnGlyLysLeuLysCysAs 69
360 TATCTGTGGGATCATTTGCATCGGGCCCAATGTCTCATGTTCACAAA 409
|||||
69 pileCysGlyIle**CysIleGlyProAsnValLeuMetValHisLys 86
410 GAAGCCACACTGGAGACGGCCCTTCAGTGCATCAATCAGTCGGGGCTCA 459
|||||
86 rgSerHisThrGlyGluArgProPheGlnCysAsnGlnCysGlyAlaSer 102
460 TTCACCCAGAGAGGCAACCTCTCCGGCACATCAAGCTGCATTCCGGGGA 509
|||||
103 PheThrGlnLysGlyAsnLeuLeuArgHisIleLysLeuHisSerGlyGI 119
510 GAAGCCCTTCAATGCCACCTCTGCAACTAGCCTGCCGCCGGAGGACG 559
|||||
119 uLysProPheLysCysHisLeuCysAsnTyrAlaCysArgArgAsp 136
560 CCCTCACTGCCACCTGAGGACGACTCCGTTGGTAAACCTCACAAATGT 609
136 laLeuThrGlyHisLeuArgThrHisSerValGlyLysProHisLysCys 152
610 GGATATTGTGGCGAAGCTATAAACAGCAGCAAGCTCTTTAGAGAAATAA 659
|||||
153 GlyTyrCysGlyArgSerTyrLysGlnArg**SerLeuGluGluHisLy 169
660 AGAGCGCTGCCAACACTACTTGGAAAGCATGGCCTTCCGGGCACACTGT 709
|||||
169 sGluArgCysHisAsnTyrLeuGluSerMetGlyLeuProGly***** 186
710 ACCAGTCATTAAAGAAGAACTAAGCACAGTGAATGGCAGAAAGACCTG 759
|||||
186 **ProValIleLysGluThr***His***GluMetAlaGluAspLeu 202
760 TGAAGATAGGATCAGAGAGATCTCTGCTGGACAGACTAGCAAGTAA 809
203 CysLysIleGly**GluArgSerLeuValLeuAspArgLeuAlaSerAs 219
810 TGTCCGCAAGCTGAGAGCTCTATGCTTCAGAAATTTCTTGGGACAAAGG 859
219 nValAlaLysArgLysSerSerMetProGlnLysPheLeuGlyAspLys 236
860 GCCTGTCCGACACGCCCTTACACAGTCCACGTACGAGAGAGAGAGAGAA 909
236 **LeuSerAsp***ProTyrAspSerAla***TyrGluLysGlu***** 252
910 ATGATGAAGTCCACGTGATGGACCAAGCCATCAACAACGCCATCAACTA 959
253 MetMet***SerHisValMetAsp***AlaIleAsnAlaIleAsnTy 269
960 CTTGGGGCCGAGTCCCTGCGCCGCTGTTGTCAGACGCCCGCCGGCGGTT 1009
269 rLeuGlyAlaGluSerLeuArgProLeuValGlnThrProProGly**** 286
1010 CCGAGGTGTTCCCGGTTCATCAGCCCGATGTACCAGCTGCAC...AGGCGC 1056
286 erGluValValProValIleSerProMetTyrGlnLeuHis***** 302
1057 TCGGAGGACCCCGCGCTCCCAACCACTCGGCCAGACAGCGCCGCTGGA 1106
303 Ser***Gly***ProArgSerAsnHisSerAlaGlnAsp***AlaVal** 319
1107 GTACCTGCTGCTCTCCAGGCCCAAGTTGGTCCCTCGGAGCGCGAGG 1156
319 ***LeuLeuLeuSerLysAlaLys***Val***SerGluArgGlu 336
1157 CTTCCCGGAGCAACAGCTGCCAAGACTCCACGACACCGAGACCAAC 1206
336 laSerProSerAsnSerCysGlnAspSerThrAspThrGluSerAsn** 352
1207 GAGGAGACCGCGGCTTATCTACTGACCAACCAACATCGCCGACG 1256
|||||

Wed Aug 28 10:05:37 2002

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353  GluGluGlnArgSerGlyLeuIleTyrLeuThrAsnHisIle***** 369
1257  CGCG...CAACGGGTGTCCTCAAGAGGACACCGCGCCTACGACCTGC 1303
    ||| ::::::::::::::| | | | | | | | | | | | | | | | | |
369  *Ala*****LeuLySGluGlu***ArgAlaTyr*****L 386
13304  TGC CGCGCGCGCTCCGAGAAGCTCGAGAGCGCGCTCCGCGTGGTCAGAC 1353
    ||| ::::::::::::::| | | | | | | | | | | | | | | | | |
386  euArgAlaAlaSerGluAsnSerGlnAspAla**ArgValValSerThr 402
13354  AGCGGGAGCAGATGAAGGTGTACAGTCCGAACACTGCCGGGTGCTCTT 1403
403  SerGlyGluGln***LysValTyrLysCysGluHisCysArgValLeuPh 419
1404  CCTGGATCAGTCTATGTACACCATCCACATG.....GGCTGCGCAG 1444
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
419  eLeuAspHisValMetTyrThrIleHisMet*****GlyCysHisG 436
1445  GCTTCGCTGATCCTTTTGTAGTCAACATGTGCGGCTACACACCGCAGGAC 1494
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
436  LysPheArgAspPropheGluCysAsnMetCysGlyTyrHisSerGlnAsp 452
1495  CGGTACGAGTTCCTCGTCGCACATAACCGAGGGGAGCACCCTTCACAT 1544
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
453  ArgTyrGluPheSerSerHisIleThrArgGlyGluHisArg***His* 469
1545  GAGC 1548
    |||
469  *Ser 470

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